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Robust biocatalysts may be formed by encapsulating prosthetic group in hydrophobic pocket like micelles, vesicles and macrocyclic compounds that mimic the polypeptide envelope protecting the catalytic center located in the natural enzymes. Artificial enzymes could biomimetically constructed from native protein as host for prosthetic active site to simulate the catalytic functions exhibited by natural enzymes. New four-component nano-biocatalyst concluding Camel β -Casein (C β -Casein), SDS, heme, imidazole, coined by us "Caseoperoxidase" provided high catalytic efficiency, as peroxidase-like nano-artificial enzyme, that was 24.5% native horseradish peroxidase (HRP). Caseoperoxidase is a biomimetic of native peroxidase that incorporates the active site by protein hydrophobic inside. Camel β -casein was selected as an appropriate apo-protein for heme active site by homology modeling method. Heme docking into new obtained camel β -casein structure indicates one heme incorporates with β -casein. Docking analysis has predicted the presence of one main active site and minor sites for heme ligand to C β -Casein. The presence of one main electrostatic site for the active-site into β -casein protein was also confirmed by experimental method through Wyman binding potential. Further experiments also confirm the retention of caseoperoxidase structure and function as artificial enzyme.

Keywords: Caseoperoxidase, Nano-artificial Enzyme, Horseradish Peroxidase (HRP), Biomimetic, Camel β -Casein, SDS, Heme.

Abstract No.178

Study of the Interaction Between Human Serum Albumin and Co (III) –Salen Complex Using Fluorescence Spectroscopy

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Distribution, metabolism and elimination of drugs, depend on the binding of drugs to protein. The characterization of molecular interactions between protein and drugs provide important clue for designing of effective drugs for the treatment of disease. Human serum albumin (HSA) is responsible protein for binding and transporting of numerous compounds, such as hormones, fatty acids and drugs. The discovery that cobalt (III) Schiff base complexes are potent antiviral agents prompted us to initiate an investigation of Co (III) interactions with proteins and nucleic acids. Co (III) Schiff base complexes with two amines in axial positions have been used as antimicrobial agents. The interaction of the Co (III)-salen complex with DNA using fluorescence Spectroscopy has been studied. Here, the interaction of Co (III)-salen of N, N'-dipyridoxyl (1, 4-butanediamine) Schiff-base complex with human serum albumin (HSA) in phosphate buffer solution has been investigated using fluorescence spectroscopy. The successive fixed amount of drug solution was added to HSA solution. Upon additions of ligand, fluorescence intensity of HSA decreased, so successive binding of the drug should occur close to tryptophan residue that causes quenching. Also a blue shift was observed, which indicated the fall of polarity and the increase of hydrophobicity around tryptophan residues. The Stern-Volmer quenching constant, $K_{sv} = 7.7 \times 10^4 \text{ M}^{-1}$ and quenching rate constant of the biomolecule, $K_q = 7.7 \times 10^{12} \text{ L mol}^{-1} \text{ s}^{-1}$ were determined using the Sterns–Volmer equation to provide a measure of the binding affinity between ligand and HSA. Also, according to the Lineweaver-Burk equation binding constant has been calculated. The results indicated that the binding between drug and HSA are strong and the possible quenching mechanism between HSA and ligand was suggested as static quenching.

Keywords: Human Serum Albumin, Cobalt (III)-Salen, Quenching, Fluorescence Spectroscopy.

Abstract No.179

Radical Scavenging Capability of Different Phenolic Acids: Caffeic, Ferulic, P-coumaric and Sinapinic Acids

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